geWorkbench

geWorkbench

geWorkbench is supported by the Molecular Analysis Tools Knowledge Center.
For more information on receiving support for this tool, please visit the Molecular Analysis Tools Knowledge Center.

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Quick Links

- MAT KC Forum
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- ICR Workspace
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Tool Overview

geWorkbench is a platform for integrated genomics, offering strong capabilities in the analysis and visualization of gene expression, sequence, and protein structure data. It offers direct access to numerous external data sources, including **caArray**, the **Cancer Gene Index** (gene-disease-compound associations), the **Cancer Gene Atlas, BioCarta** and the **Pathway Interaction Database**, as well as to sequence, molecular interaction, and structural databases. Written in Java for use on the desktop, geWorkbench is open-source and cross-platform, and has an extensible, component-based architecture. geWorkbench is supported by an active development effort.

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What's New

For news and events, visit What's new for geWorkbench.

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At A Glance Details

Current Version Number: 2.2.2
Release Date of Current Version: August 19, 2011
Intended Audiences: Biomedical research practitioners
Primary Workspace: ICR
Currently caGrid Enabled? Yes (5 analytical services)
caBIG® compatibility Level: Silver

Technical Information

Tool Maturity Assessment: Stable Release (Adoption in Progress)
Installation Level: Intermediate - technical assistance may be required, download may require supporting infrastructure or software

System Requirements

geWorkbench is a desktop application providing access to remote data and analysis services. geWorkbench is downloaded as a self-installing package with support for Windows, Linux and MAC OS-X. To achieve reasonable performance when using realistic data sets, a system configuration with at least 2 GB of RAM is recommended.

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Presentations, Demos and Other Materials

- geWorkbench overview at the AACR 2011 Annual Meeting
- geWorkbench Introductory Video (applicable up to geWorkbench 1.7.0) (make sure your speakers are on to play audio)
- geWorkbench Brochures

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Documentation, Meeting and Training

geWorkbench Meetings and Plans

- geWorkbench Roadmap

geWorkbench Documentation

End User	Technical	Download and Sample Data
• User tutorials • Sample Screenshots • geWorkbench Training Manual • geWorkbench Project Site	• Installation Requirements • Installation FAQ • geWorkbench Known issues • Developer's Page	• geWorkbench download area • geWorkbench Tutorial Sample Data • Bcell-100 Sample Data

geWorkbench Knowledge Base

Visit geWorkbench FAQ and In-depth Articles to find the answers to the most frequently asked questions and develop understanding of how geWorkbench works.

Visit geWorkbench Demos for an in-depth look at operation of geWorkbench.

Refer to geWorkbench Biological Scenarios to see geWorkbench in action and how to apply geWorkbench to your real biological scenarios.

geWorkbench Case Studies

If you still don't know if geWorkbench is for you, review the Case studies to see examples of how geWorkbench could be used in different scenarios.

geWorkbench Citations

Refer to geWorkbench Citations for a list of articles about geWorkbench.

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Installation and Downloads

- Download, Install or Upgrade geWorkbench
- geWorkbench plugins

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Forum and Support for geWorkbench

Forum	Support	Archived Info
• End User Forum • Developer Forum	• Link to NCI gForge site for geWorkbench: geWorkbench at NCI gForge • ICR Workspace Coordinator: Elaine Freund efreund at 3rdmill.com • NCICB Applications Support: ncicb@pop.nci.nih.gov	–

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Submit defects and feature requests for geWorkbench

- Report a Defect or Request a Feature for geWorkbench at Jira
- Official geWorkbench Bug and Feature Report tracked @ Mantis

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Open-source development

- Link to geWorkbench Open Development Code Base (svn)
- geWorkbench developer's corner

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Integration with other tools - caArray

geWorkbench can query for data in an instance of caArray via a Java API. Several operations are supported. You can:

1. Query for experiments, for example by platform or by species
2. Select from which hybridizations in an experiment you wish to download data
3. Download derived (summarized, probeset-level) data that has been parsed into the database. An example is the values loaded from Affymetrix CHP files (created through GCOS/MAS5). geWorkbench does not currently support retrieving or analyzing Affy CEL files directly.

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